

RAW SEQUENCE LISTING

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Application Serial Number: 10/507,132
Source: PCT
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RAW SEQUENCE LISTING

DATE: 04/11/2006

PATENT APPLICATION: US/10/507,132

TIME: 12:29:51

Input Set : A:\2005-06-06 1254-0258PUS1.ST25.txt

Output Set: N:\CRF4\04112006\J507132.raw

3 <110> APPLICANT: Koichiro KAKU et al.

5 <120> TITLE OF INVENTION: GENE CODING FOR SCYTALONE DEHYDRATASE EXHIBITING RESISTANCE

TO

6 AGRICULTURAL FUNGICIDAL AGENT

8 <130> FILE REFERENCE: 1254-0258PUS1

10 <140> CURRENT APPLICATION NUMBER: US 10/507,132

11 <141> CURRENT FILING DATE: 2004-09-10

13 <150> PRIOR APPLICATION NUMBER: JP 2002-66955

14 <151> PRIOR FILING DATE: 2002-03-12

16 <160> NUMBER OF SEQ ID NOS: 19

18 <170> SOFTWARE: Patentin Ver. 2.1

20 <210> SEQ ID NO: 1

21 <211> LENGTH: 516

22 <212> TYPE: DNA

23 <213> ORGANISM: Pyricularia oryzae

25 <220> FEATURE:

26 <221> NAME/KEY: CDS

27 <222> LOCATION: (1)..(516)

29 <400> SEQUENCE: 1

30 atg ggt tcg caa gtt caa aag agc gat gag ata acc ttc tca gac tac 48

31 Met Gly Ser Gln Val Gln Lys Ser Asp Glu Ile Thr Phe Ser Asp Tyr

32 1 5 10 15

34 ctg ggc ctc atg act tgc tat gag tgg gca gac agc tac gac tcc 96

35 Leu Gly Leu Met Thr Cys Val Tyr Glu Trp Ala Asp Ser Tyr Asp Ser

36 20 25 30

38 aag gac tgg gat agg ctg cga aag gtc att gcg cct act ctg cgc att 144

39 Lys Asp Trp Asp Arg Leu Arg Lys Val Ile Ala Pro Thr Leu Arg Ile

40 35 40 45

42 gac tac cgc tcc ttc ctc gac aag ctc tgg gag gca atg ccg gcc gag 192

43 Asp Tyr Arg Ser Phe Leu Asp Lys Leu Trp Glu Ala Met Pro Ala Glu

44 50 55 60

46 gag ttc gtc ggc atg gtc agc aag cag atg ctg ggc gac ccc acc 240

47 Glu Phe Val Gly Met Val Ser Ser Lys Gln Met Leu Gly Asp Pro Thr

48 65 70 75 80

50 ctc cgc acg cag cac ttc atc ggc ggc acg cgc tgg gag aag gtg tcc 288

51 Leu Arg Thr Gln His Phe Ile Gly Gly Thr Arg Trp Glu Lys Val Ser

52 85 90 95

54 gag gac gag gtc atc ggc tac cac cag ctg cgc gtc ccg cac cag agg 336

55 Glu Asp Glu Val Ile Gly Tyr His Gln Leu Arg Val Pro His Gln Arg

56 100 105 110

58 tac aag gac acc acc atg aag gag gtc acc atg aag ggc cac gcc cac 384

59 Tyr Lys Asp Thr Thr Met Lys Glu Val Thr Met Lys Gly His Ala His

60 115 120 125

62 tcg gca aac ctt cac tgg tac aag aag atc gac ggc gtc tgg aag ttc 432

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63 Ser Ala Asn Leu His Trp Tyr Lys Lys Ile Asp Gly Val Trp Lys Phe
 64 130 135 140
 66 gcc ggc ctc aag ccc gat atc cgc tgg ggc gag ttc gac ttt gac agg 480
 67 Ala Gly Leu Lys Pro Asp Ile Arg Trp Gly Glu Phe Asp Phe Asp Arg
 68 145 150 155 160
 70 atc ttt gag gac gga cgg gag acc ttt ggc gac aaa 516
 71 Ile Phe Glu Asp Gly Arg Glu Thr Phe Gly Asp Lys
 72 165 170
 75 <210> SEQ ID NO: 2
 76 <211> LENGTH: 172
 77 <212> TYPE: PRT
 78 <213> ORGANISM: Pyricularia oryzae
 80 <400> SEQUENCE: 2
 81 Met Gly Ser Gln Val Gln Lys Ser Asp Glu Ile Thr Phe Ser Asp Tyr
 82 1 5 10 15
 84 Leu Gly Leu Met Thr Cys Val Tyr Glu Trp Ala Asp Ser Tyr Asp Ser
 85 20 25 30
 87 Lys Asp Trp Asp Arg Leu Arg Lys Val Ile Ala Pro Thr Leu Arg Ile
 88 35 40 45
 90 Asp Tyr Arg Ser Phe Leu Asp Lys Leu Tip Gln Ala Met Pro Ala Glu
 91 50 55 60
 93 Glu Phe Val Gly Met Val Ser Ser Lys Gln Met Leu Gly Asp Pro Thr
 94 65 70 75 80
 96 Leu Arg Thr Gln His Phe Ile Gly Gly Thr Arg Trp Glu Lys Val Ser
 97 85 90 95
 99 Glu Asp Glu Val Ile Gly Tyr His Gln Leu Arg Val Pro His Gln Arg
 100 100 105 110
 102 Tyr Lys Asp Thr Thr Met Lys Glu Val Thr Met Lys Gly His Ala His
 103 115 120 125
 105 Ser Ala Asn Leu His Trp Tyr Lys Lys Ile Asp Gly Val Trp Lys Phe
 106 130 135 140
 108 Ala Gly Leu Lys Pro Asp Ile Arg Trp Gly Glu Phe Asp Phe Asp Arg
 109 145 150 155 160
 111 Ile Phe Glu Asp Gly Arg Glu Thr Phe Gly Asp Lys
 112 165 170
 116 <210> SEQ ID NO: 3
 117 <211> LENGTH: 516
 118 <212> TYPE: DNA
 119 <213> ORGANISM: Pyricularia oryzae
 121 <220> FEATURE:
 122 <221> NAME/KEY: CDS
 123 <222> LOCATION: (1)..(516)
 125 <400> SEQUENCE: 3
 126 atg ggt tcg caa gtt caa aag agc gat gag ata acc ttc tca gac tac 48
 127 Met Gly Ser Gln Val Gln Lys Ser Asp Glu Ile Thr Phe Ser Asp Tyr
 128 1 5 10 15
 130 ctg ggc ctc atg act tgc gtc tat gag tgg gca gac agc tac gac tcc 96
 131 Leu Gly Leu Met Thr Cys Val Tyr Glu Trp Ala Asp Ser Tyr Asp Ser
 132 20 25 30

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134 aag gac tgg gat agg ctg cga aag gtc att gcg cct act ctg cgc att	144
135 Lys Asp Trp Asp Arg Leu Arg Lys Val Ile Ala Pro Thr Leu Arg Ile	
136 35 40 45	
138 gac tac cgc tcc ttc ctc gac aag ctc tgg gag gca atg ccg gcc gag	192
139 Asp Tyr Arg Ser Phe Leu Asp Lys Leu Trp Glu Ala Met Pro Ala Glu	
140 50 55 60	
142 gag ttc gtc ggc atg gtc tcg agc aag cag gtg ctg ggc gac ccc acc	240
143 Glu Phe Val Gly Met Val Ser Ser Lys Gln Val Leu Gly Asp Pro Thr	
144 65 70 75 80	
146 ctc cgc acg cag cac ttc atc ggc ggc acg cgc tgg gag aag gtg tcc	288
147 Leu Arg Thr Gln His Phe Ile Gly Gly Thr Arg Trp Glu Lys Val Ser	
148 85 90 95	
150 gag gac gag gtc atc ggc tac cac cag ctg cgc gtc ccg cac cag agg	336
151 Glu Asp Glu Val Ile Gly Tyr His Gln Leu Arg Val Pro His Gln Arg	
152 100 105 110	
154 tac aag gac acc acc atg aag gag gtc acc atg aag ggc cac gcc cac	384
155 Tyr Lys Asp Thr Thr Met Lys Glu Val Thr Met Lys Gly His Ala His	
156 115 120 125	
158 tgg gca aac ctt cac tgg tcc aag aac atc gac ggc gtc tgg aag ttc	432
159 Ser Ala Asn Leu His Trp Tyr Lys Ile Asp Gly Val Trp Lys Phe	
160 130 135 140	
162 gcc ggc ctc aag ccc gat atc cgc tgg ggc gag ttc gac ttt gac agg	480
163 Ala Gly Leu Lys Pro Asp Ile Arg Trp Gly Glu Phe Asp Phe Asp Arg	
164 145 150 155 160	
166 atc ttt gag gac gga cgg gag acc ttt ggc gac aaa	516
167 Ile Phe Glu Asp Gly Arg Glu Thr Phe Gly Asp Lys	
168 165 170	
171 <210> SEQ ID NO: 4	
172 <211> LENGTH: 172	
173 <212> TYPE: PRT	
174 <213> ORGANISM: Pyricularia oryzae	
176 <400> SEQUENCE: 4	
177 Met Gly Ser Gln Val Gln Lys Ser Asp Glu Ile Thr Phe Ser Asp Tyr	
178 1 5 10 15	
180 Leu Gly Leu Met Thr Cys Val Tyr Glu Trp Ala Asp Ser Tyr Asp Ser	
181 20 25 30	
183 Lys Asp Trp Asp Arg Leu Arg Lys Val Ile Ala Pro Thr Leu Arg Ile	
184 35 40 45	
186 Asp Tyr Arg Ser Phe Leu Asp Lys Leu Trp Glu Ala Met Pro Ala Glu	
187 50 55 60	
189 Glu Phe Val Gly Met Val Ser Ser Lys Gln Val Leu Gly Asp Pro Thr	
190 65 70 75 80	
192 Leu Arg Thr Gln His Phe Ile Gly Gly Thr Arg Trp Glu Lys Val Ser	
193 85 90 95	
195 Glu Asp Glu Val Ile Gly Tyr His Gln Leu Arg Val Pro His Gln Arg	
196 100 105 110	
198 Tyr Lys Asp Thr Thr Met Lys Glu Val Thr Met Lys Gly His Ala His	
199 115 120 125	
201 Ser Ala Asn Leu His Trp Tyr Lys Lys Ile Asp Gly Val Trp Lys Phe	

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202 130 135 140
 204 Ala Gly Leu Lys Pro Asp Ile Arg Trp Gly Glu Phe Asp Phe Asp Arg
 205 145 150 155 160
 207 Ile Phe Glu Asp Gly Arg Glu Thr Phe Gly Asp Lys
 208 165 170
 211 <210> SEQ ID NO: 5
 212 <211> LENGTH: 21
 213 <212> TYPE: DNA
 214 <213> ORGANISM: Artificial Sequence
 216 <220> FEATURE:
 217 <223> OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized
 primer
 219 <400> SEQUENCE: 5
 220 gcagtgtataccacacaaa g 21
 223 <210> SEQ ID NO: 6
 224 <211> LENGTH: 22
 225 <212> TYPE: DNA
 226 <213> ORGANISM: Artificial Sequence
 228 <220> FEATURE:
 229 <223> OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized
 primer
 231 <400> SEQUENCE: 6
 232 ttattttgtcg gcaaaggctt cc 22
 235 <210> SEQ ID NO: 7
 236 <211> LENGTH: 44
 237 <212> TYPE: DNA
 238 <213> ORGANISM: Artificial Sequence
 240 <220> FEATURE:
 241 <223> OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized
 primer
 243 <400> SEQUENCE: 7
 244 agttcgaact ggaattcaac cggcacgcatttgcatttttca 44
 247 <210> SEQ ID NO: 8
 248 <211> LENGTH: 21
 249 <212> TYPE: DNA
 250 <213> ORGANISM: Artificial Sequence
 252 <220> FEATURE:
 253 <223> OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized
 primer
 255 <400> SEQUENCE: 8
 256 atgggttcgc aagttcaaaa g 21
 259 <210> SEQ ID NO: 9
 260 <211> LENGTH: 23
 261 <212> TYPE: DNA
 262 <213> ORGANISM: Artificial Sequence
 264 <220> FEATURE:
 265 <223> OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized
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 267 <400> SEQUENCE: 9
 268 gtggcccttc atggtgaccc tct 23
 271 <210> SEQ ID NO: 10
 272 <211> LENGTH: 20
 273 <212> TYPE: DNA

274 <213> ORGANISM: Artificial Sequence

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276 <220> FEATURE:
 277 <223> OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized
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 279 <400> SEQUENCE: 10 20
 280 acaagctctg ggaggcaatg
 283 <210> SEQ ID NO: 11
 284 <211> LENGTH: 37
 285 <212> TYPE: DNA
 286 <213> ORGANISM: Artificial Sequence
 288 <220> FEATURE:
 289 <223> OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized
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 291 <400> SEQUENCE: 11 37
 292 atcgtcagc tgaattcg tc ttgtaaaagc cgccaaac
 295 <210> SEQ ID NO: 12
 296 <211> LENGTH: 27
 297 <212> TYPE: DNA
 298 <213> ORGANISM: Artificial Sequence
 300 <220> FEATURE:
 301 <223> OTHER INFORMATION: Description of Artificial Sequence: chemically synthesized
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 303 <400> SEQUENCE: 12 27
 304 ttctgtcgca tggcttcgag catctag
 307 <210> SEQ ID NO: 13
 308 <211> LENGTH: 600
 309 <212> TYPE: DNA
 310 <213> ORGANISM: Pyricularia oryzae
 312 <400> SEQUENCE: 13
 313 ctagcaaccg cagtatacc cacaccaaag agttccattc agtcttagtat agttcacttc 60
 315 aactttaaa agccgccaac atgggttcgc aagtcaaaa gagcgatgag ataaccttct 120
 317 cagactaccc gggccatcg acttgcgtct atgagtgccc agacagctac gactccaagg 180
 319 actgggatag gctgcgaaaag gtcattgcgc ctactctgcg cattgactac cgcccttcc 240
 321 tcgacaagct ctgggaggca atgcccggcgc aggagttcg tggcatggc tcgagcaagc 300
 323 aggtgctggg cgacccacc ctccgcacgc agcacttcat cggcggcacg cgctgggaga 360
 325 aggtgtccga ggacgagggtc atcggctacc accagctgcg cgtccgcac cagaggtaca 420
 327 aggacaccac catgaaggag gtcaccatga agggccacgc ccactcgca aacccact 480
 329 ggtacaagaa gatcgacggc gtctggaaat tcgcggcct caagcccgt atccgctggg 540
 331 gcgagttcga ctttgacagg atctttgagg acggacggga gaccttggc gacaaataaaa 600
 334 <210> SEQ ID NO: 14
 335 <211> LENGTH: 545
 336 <212> TYPE: DNA
 337 <213> ORGANISM: Pyricularia oryzae
 339 <400> SEQUENCE: 14
 340 ctagtatagt tcacttcaac ttgtaaaagc cgccaaatcg ggttcgcaag ttcaaaagag 60
 342 ccatgagata accttctcg actacctggg cctcatgact tgcgtctatg agtgggcaga 120
 344 cagctacgac tccaaaggact gggataggct gcgaaagggtc attgcgccta ctctgcgcac 180
 346 tgactaccgc tccttcctcg acaagctcg ggaggcaatg cggccggagg agtgcgtcgg 240
 348 catggtctcg agcaagcagg tgctggcga cccaccctc cgcacgcacg acttcattcg 300
 350 cggcacgcgc tgggagaagg tgcggagga cgaggtcattt ggctaccacc agtgcgcgt 360
 352 cccgcaccag aggtacaagg acaccaccaat gaaggagggtc accatgaagg gccacgccc 420
 354 ctcggcaaac cttcaactggt acaagaagat cgacggcgtc tggaaatcg ccggcctcaa 480
 356 gccccacatc cgctgggacg agttcgactt tgacaggatc tttgaggacg gacgggagac 540

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